

GenCore version 4.5
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OM nucleic - nucleic search, using sw model
Run on: May 14, 2001, 18:24:52 ; Search time 1113.17 Seconds
(without alignments)
225.225 Million cell updates/sec

Title: US-09-373-230-5
Perfect score: 17
Sequences: 1. TTYGARGARATGGAYCC 17
Scoring table: IDENTITY_NUC
GapOp 10.0 , GapExt 1.0
Searched: 1283235 seqs, 7373929652 residues
Total number of hits satisfying chosen parameters: 2566470
Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :	GenEmbl:	*
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	2:	gb_ba2:*
	3:	gb_ba3:*
	4:	gb_in1:*
	5:	gb_in2:*
	6:	gb_in3:*
	7:	gb_on:*
	8:	gb_ox:*
	9:	gb_patt1:*
	10:	gb_Pat2:*
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	12:	gb_Pl1:*
	13:	gb_Pl2:*
	14:	gb_Pl3:*
	15:	gb_Pl4:*
	16:	em_ba1:*
	17:	em_ba2:*
	18:	em_tun:*
	19:	em_ntgo_hum:*
	20:	em_ntgo_inv:*
	21:	em_ntgo_rnd:*
	22:	em_ntq_hum1:*
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	25:	em_ntq_hum4:*
	26:	em_ntq_hum5:*
	27:	em_ntq_hum6:*
	28:	em_ntq_hum7:*
	29:	em_ntq_hum8:*
	30:	em_ntq_inv1:*
	31:	em_ntq_inv2:*
	32:	em_ntq_othe:*
	33:	em_ntq_rnd:*
	34:	em_hum1:*
	35:	em_hum2:*
	36:	em_hum3:*
	37:	em_hum4:*
	38:	em_hum5:*
	39:	em_hum6:*
	40:	em_hum7:*
	41:	em_in:*
	42:	em_on:*
	43:	em_oI:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	15.4	90.6	17 9 AR072047	AR072047 Sequence
2	15.4	90.6	471 9 AR072044	AR072044 Sequence
3	15.4	90.6	471 10 E13264	Mouse cDNA
4	15.4	90.6	471 10 E14257	cDNA encodi
5	15.4	90.6	471 10 E14760	E14760 cDNA encodi
6	15.4	90.6	471 10 E17139	E17139 Murine mRNA
7	15.4	90.6	471 45 E10609	E10609 Mouse cDNA
8	15.4	90.6	471 45 E11744	E11744 cDNA encodi
9	15.4	90.6	471 45 E12010	E12010 cDNA encodi
10	15.4	90.6	471 56 Y02278	Artificial
11	15.4	90.6	572 94 MM66244	Mus musculu

RESULT	1	REFERENCE	D49494	Mouse mRNA	LOCUS	AR072044	471 bp	DNA	PAT	18-FEB-2000
AR072047		AUTHORS	AP000229	Homo sapi	DEFINITION	Sequence 1 from patent US 5912324.				
LOCUS	AR072047	DEFINITION	AP000229	Homo sapi	ACCESSION	AR072044				
DEFINITION	Sequence 5 from patent	VERSION	AC080029	Homo sapi	VERSION	AR072044.1	GI:7222932			
ACCESSION	AR072047	KEYWORDS	AC080029	Homo sapi	SOURCE	Unknown.				
VERSION	AR072047.1	JOURNAL	AC080029	Homo sapi	ORGANISM	Unclassified.				
KEYWORDS		FEATURES	AC080029	Homo sapi	REFERENCE	1 (bases 1 to 471)				
SOURCE	Unknown.	source	AC080029	Homo sapi	AUTHORS	Okamura, H., Tanimoto, T., Torigoe, K., Kunikata, T., Taniguchi, M., Kohno, K. and Kurimoto, M.,				
ORGANISM	Unclassified.	mat_peptide	AC080029	Homo sapi	TITLE	Interferon-gamma (IFN-gamma.) inducing factor (IGIF, IL-18)				
REFERENCE	1 (bases 1 to 17)	product	AC080029	Homo sapi	JOURNAL	Patent; US 5912324-A 15-JUN-1999;				
AUTHORS	Okamura, H., Tanimoto, T., Torigoe, K., Kunikata, T., Taniguchi, M., Kohno, K. and Kurimoto, M.,	source	AC080029	Homo sapi	FEATURES	Location/Qualifiers				
TITLE	Interferon-gamma (IFN-gamma.) inducing factor (IGIF, IL-18)	mat_peptide	AC080029	Homo sapi	SOURCE	1. .471				
JOURNAL	Patent; US 5912324-A 15-JUN-1999;	product	AC080029	Homo sapi	BASE COUNT	162 a	91 c	92 g	125 t	1 others
FEATURES	Location/Qualifiers	source	AC080029	Homo sapi	ORIGIN					
SOURCE	1. .471	base	AC080029	Homo sapi	Query Match	Best Local Similarity	90.6%	Score	15.4;	DB 9;
BASE COUNT	4 a	length	AC080029	Homo sapi	Matches	76.5%	pred.	No.	4	5e+02;
ORIGIN	2 c	indels	AC080029	Homo sapi	Mismatches	4;	Indels	0;		Gaps 0;
Query Match	49	gaps	AC080029	Homo sapi	Db	244	TITGAGGAATGGATCC	260		
RESULTS	12	LOCUS	EL3264	471 bp	DEFINITION	Mouse cDNA encoding a protein that induces to produce				
RESULT	1	KEYWORDS	EL3264	DNA	ACCESSION	EL3264-1 GI:3252069				
RESULT	1	ORGANISM	EL3264	interferon-gamma.	VERSION	EL3264-1 GI:3252069				
RESULT	1	REFERENCE	EL3264	mouse	KEYWORDS	JP 1997157180-A/2.				
RESULT	1	AUTHORS	EL3264	cDNA	ORGANISM	Mus sp.				
RESULT	1	TITLE	EL3264	encoding	REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Murida; Murinae; Mus.				
RESULT	1	JOURNAL	EL3264	a protein	AUTHORS	Torigoe, K., Tanimoto, T., Fukuda, S. and Kurimoto, M.				
RESULT	1	FEATURES	EL3264	that induces	TITLE	AGENT FOR SENSITIVE DISEASE				
RESULT	1	SOURCE	EL3264	to produce	JOURNAL	PATENT: JP 1997157180-A 2-17-JUN-1997;				
RESULT	1	COMMENT	EL3264		COMMENT	HAYASHIBARA BIOCHEM LAB INC				
RESULT	1	REFERENCE	EL3264		OS	Mus sp. (mouse)				
RESULT	1	AUTHORS	EL3264		PN	JP 1997157180-A/2				
RESULT	1	TITLE	EL3264		PD	JP 1997-1997				
RESULT	1	JOURNAL	EL3264		PF	24-JAN-1996				
RESULT	1	FEATURES	EL3264		PR	10-MAR-1995				
RESULT	1	SOURCE	EL3264		04-OCT-1995	JP 95P 78357, 29-SEP-1995				
RESULT	1	COMMENT	EL3264		PI	JP 95P 78306				
RESULT	1	REFERENCE	EL3264		KURIMOTO, MASASHI	TORIGOE, KAKUJI, TANIMOTO, TADAO, FUKUDA, SHIGEATSU, PI				
RESULT	1	AUTHORS	EL3264		KURIMOTO, MASASHI					
RESULT	1	TITLE	EL3264		KURIMOTO, MASASHI					
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QY 1 TTGARGARATGGAYCC 17
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Db 244 TTGGAGAATGGACCC 260

RESULT 9

ID E12010 standard; RNA; ROD; 471 BP.

XX E12010:
AC E12010:
XX E12010.1
SV E12010.1
XX 07-OCT-1997 (Rel. 52, Created)
DT 02-SEP-2000 (Rel. 65, Last updated, Version 2)

DE CDNA encoding mouse polypeptide which introduce interferon-gamma product in immunocompetent cell.

XX JP 199631598-A/2.

OS Mus musculus (house mouse)
OC Eutheria; Rodentia; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
XX Eukaryota; Metazoa;
RN [1]
RP 1-471
RA Kunikata T., Taniguchi M., Kono K., Kurimoto M.;
RT "MONOCLONAL ANTIBODY";
RL Patent number: JP199631598-A/2, 10-SEP-1996.
RL HAYASHIBARA BIOCHEM LAB INC.
XX OS Mus musculus (mouse)
CC PN JP 199631598-A/2
CC PD 10-SEP-1996
CC PF 23-FEB-1995 JP 1995058240
CC PI KUNIKATA TOSHIO, TANIGUCHI MITSUKO, KONO KEIZO,
KURIMOTO MASASHI
PC C07K16/24, C07K11/16, C07K11/18, C07K11/22, C07K11/26, C07K11/30,
CC C07K11/34, C12N5/10,
CC PC C12N15/02, C12P21/08, G01N33/53, G01N33/57//A61K38/21, A61K39/395,
CC PC C12P21/08,
CC PC C12K11/91;
CC CC strandness: Double;
CC CC topology: linear;
CC CC hypothetical: No;
CC CC anti-sense: No;
FH Key
FH source 1. .471
FT source /organism="Mus musculus"
XX Location/Qualifiers
FH Key
FH source 1. .471
FT source /db_xref="taxon:10090"
/tissue_type="liver"
SQ Sequence 471 BP; 162 A; 91 C; 92 G; 125 T; 1 other;

Query Match 90.6%; Score 15.4; DB 56; Length 471;
Best Local Similarity 76.5%; Pred. No. 4; 5e+02; 0;
Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
Version 1.13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

RESULT 11

MM066244 MM066244 572 bp mRNA ROD 18-MAR-1997
LOCUS MM066244 Mus musculus interferon-gamma inducing factor mRNA, partial cds.
DEFINITION Mus musculus interferon-gamma inducing factor mRNA, partial cds.
ACCESSION U66244
VERSION U66244.1 GI:1561735

KEYWORDS

SOURCE house mouse.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciuognathi; Muridae; Mus.

REFERENCE 1 (bases 1 to 572)
AUTHORS Rotte, H., Jenkins, N.A., Copeland, N.G. and Kolb, H.
TITLE Active stage of autoimmune diabetes is associated with the expression of a novel cytokine, IGF, which is located near Id2 gene.
JOURNAL J. Clin. Invest. 99 (3), 469-474 (1997)
MEDLINE 97174346
REFERENCE 2 (bases 1 to 572)
AUTHORS Rotte, H., Copeland, N.G. and Kolb, H.
TITLE Direct Submission
JOURNAL Submitted (06-AUG-1996) Diabetes Research Institute, Auf#m Henniekamp 65, Dusseldorf 40225, Germany
FEATURES source
Location/Qualifiers 1. .572
/organism="Mus musculus"
/strain="non obese diabetic (NOD)"
/db_xref="taxon:10090"
/chromosome="9"
/tissue_type="pancreas"

QY 1 TTGARGARATGGAYCC 17
||:|||||:
Db 244 TTGGAGAATGGACCC 260

Sequence Match Similarity 90.6%; Score 15.4; DB 45; Length 471;
Best Local Similarity 76.5%; Pred. No. 4; 5e+02; 0;
Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGARGARATGGAYCC 17
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Db 244 TTGGAGAATGGACCC 260

RESULT 10

CDS

1. >572
 /note="IGIF"
 /codon_start=1
 /product="interferon gamma inducing factor"
 /protein_id="BAA8753_1."
 /db_xref="GI:1561736"
 /translation="MAAMSEDSCNFKEMFINTLYFPEENGDLSDNFGRHLCTT
 AVIRVINDQFLVVKRQPVFEDMDIDOSASEQTRLTYMVKSEVERGLATLTSVKD
 SKMSLCKNKTSFEEDPENIDDQLFQKRVPGHNMKEFESSLYBGFHLAC
 QKEDDAFKLILKKDKDENGDKSVMFTNLHQ"

BASE COUNT

196 a 111 c 113 g 152 t

ORIGIN

QY 1 TTGARGARATGGAYCC 17
 ||:||:||:||:||:||:||

Db 513 TTGAGGAATGGATCC 529

RESULT 13

AP000229/c AP000229 35143 bp DNA PRI
 LOCUS Homo sapiens genomic DNA, chromosome 21q21.1-q21.2, clone:T1539,
 DEFINITION LUS6-APP region, complete sequence.

ACCESSION AP000229

VERSION AP000229.2 GI:7262565

KEYWORDS HTG.

SOURCE Homo sapiens DNA, clone:T1539.
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 35143)
 AUTHORS Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
 Fujiyama,A., Yada,T., Tokoki,Y. and Sakaki,Y.

TITLE

JOURNAL

Masahira Hattori, The Institute of Physical and Chemical Research
 (RIKEN), Genomic Sciences Center (GSC); Kitasato Univ., 1-15-1
 Kitasato, Sagamihara, Kanagawa 228-8555, Japan
 (E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/)

Tel:81-42-778-9923, Fax:81-42-778-9924)

On Mar 17, 2000 this sequence version replaced gi:4835598.

Sequence updated (15-Mar-2000)

The sequence is a part of the data (ACCESSION No. AP000136 - AP000145).

The sequencing project is supported by Japan Science Technology Corporation (JST) and The Institute of Physical and Chemical Research (RIKEN). Location/Qualifiers

FEATURES

source

Makogawa, Hyogo College of Medicine, Department of Bacteriology;
 Mukogawa 1-11, Nishinomiyama, Hyogo 663, Japan (Tel:0798-45-6111)

COMMENT

2 (bases 1 to 866)
 Okamura, H., Tsutui,H., Komatsu,T., Yutsudo,M., Hakura,A.,
 Tanimoto,T., Torigoe,K., Okura,T., Nukada,Y., Hattori,K., Akita,K.,
 Namba,M., Tanabe,F., Konishi,K., Fukuda,S. and Kurimoto,M.

TITLE Cloning of a new cytosine that induces IFN-gamma production by T
 cells
 JOURNAL Nature 378 (6552), 88-91 (1995)
 MEDLINE 96061009
 FEATURES source
 1. .866
 /organism="Mus musculus"
 /db_xref="taxon:0090"
 /tissue_type="liver"
 1. .866
 /note="Interferon-gamma inducing factor (IGIF) mRNA"
 CDS 165 .743
 /codon_start=1
 /product="IGIF precursor polypeptide"
 /protein_id="BAA8705_1"
 /db_xref="GI:1064823"
 /translation="MAAMSEDSCNFKEMFINTLYFPEENGDLSDNFGRHLCTT
 AVIRVINDQFLVVKRQPVFEDMDIDOSASEQTRLTYMVKSEVERGLATLTSVKD
 SKMSLCKNKTSFEEDPENIDDQLFQKRVPGHNMKEFESSLYBGFHLAC
 QKEDDAFKLILKKDKDENGDKSVMFTNLHQ"

RESULT 14

Query Match 90.6%; Score 15.4; DB 94; Length 866;
 Best Local Similarity 76.5%; Pred No. 4.7e+02;
 Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

BASE COUNT

262 a 187 c 187 g 230 t

ORIGIN

BASE COUNT

10208 a 7036 c 7565 g 10334 t

ORIGIN

Query Match 90.6%; Score 15.4; DB 90; Length 35143;

Best Local Similarity 76.5%; Pred No. 6.5e+02;
 Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGARGARATGGAYCC 17

Db 25608 TTGAGGAATGGATCC 25592

RESULT 14

AC080029 AC080029 59955 bp DNA HTG
 DEFINITION Homo sapiens chromosome 4 clone CTD-2353K2 map 4, LOW-PASS SEQUENCE

ACCESSION SAMPLING

AC080029 AC080029.1 GI:10280784

VERSION

KEYWORDs HTG; HTGS_PHASE.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 5955)
 AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.

Query Match 90.6%; Score 15.4; DB 94; Length 866;
 Best Local Similarity 76.5%; Pred No. 4.7e+02;
 Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

TITLE Homo sapiens chromosome 4, clone CTD-2353K2
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 59955)
 AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
 Anderson,S., Barna,N., Bastien,V., Beda,F., Bouaslakki,L.,
 Boultzalier,B., Brown,A., Burkett,G., Campopiano,A., Castle,A.,
 Choate,J., Coangalo,M., Collins,S., Collymore,A., Cooke,P.,
 DeAngelis,R., Dewar,K., Diaz,J.S., Dodge,S., Ferreira,P.,
 FitzHugh,W., Gade,D., Galagan,J., Gardyne,S., Ginder,S., Goette,M.,
 Graham,L., Grand-Pierre,N., Hagos,B., Heaford,A., Horton,L.,
 Iliev,I., Johnson,R., Jones,C., Kahn,L., Karatas,A., Larocque,K.,
 Lazarcos,R., Landers,T., Lebocky,J., Levine,R., Lileu,C., Liu,G.,
 Macdonald,P., Marquis,N., McCarthy,M., McEwan,P., Mokeran,K.,
 McPheeters,R., Melidim,J., Meneus,L., Minova,T., Mlenga,V.,
 Morrow,J., Murphy,T., Naylor,J., Norman,C.H., O'Connor,T.,
 O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K.,
 Pierre,N., Pisani,C., Pollara,V., Raymond,C., Rieback,M., Riley,R.,
 Rogov,P., Rothman,D., Roy,A., Santos,R., Schauer,S., Severy,P.,
 Sounez,C., Spencer,B., Stange-Thomann,N., Stoianovic,N.,
 Strauss,N., Subramanian,A., Talama,J., Testayre,S., Theodore,J.,
 Turrell,A., Travers,M., Trigilio,J., Vassiliev,H., Viel,R., Vo,A.,
 Wilson,B., Wu,X., Wymand,D., Ye,W.J., Young,G., Zainoun,J.,
 Zimmer,A., and Zody,M.
 DIRECTOR
 JOURNAL Submitted (23-SEP-2000) Whitehead Institute/MIT Center for Genome Research
 COMMENT All repeats were identified using RepeatMasker:
 http://www-genome.washington.edu/RM/RepeatMasker.html
 CONTACT Center: Whitehead Institute/MIT Center for Genome Research
 Center code: WIBR
 Research, 320 Charles Street, Cambridge, MA 02111, USA
 Web site: <http://www-seq.wi.mit.edu>
 Contact: sequence_submissions@genome.wi.mit.edu
 Project Information
 Center project name: L10743
 Center clone name: 2353_K_2

* NOTE: This record contains 74 individual sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will be preserved.

1 645: contig of 645 bp in length
 * 646: 715: gap of 100 bp
 * 746: 1464: contig of 719 bp in length
 * 1465: 1664: gap of 100 bp
 * 1565: 2115: contig of 759 bp in length
 * 2316: 2415: gap of 100 bp
 * 3059: contig of 644 bp in length
 * 3060: 3159: gap of 100 bp
 * 3160: 3177: contig of 718 bp in length
 * 3878: 3977: gap of 100 bp
 * 3978: 4722: contig of 745 bp in length
 * 4723: 4822: gap of 100 bp
 * 4823: 5579: contig of 757 bp in length
 * 5580: 5679: gap of 100 bp
 * 5680: 6315: contig of 636 bp in length
 * 6316: 6415: gap of 100 bp
 * 6416: 7240: contig of 865 bp in length
 * 7281: 7380: gap of 100 bp
 * 7381: 8134: contig of 754 bp in length
 * 8135: 8234: gap of 100 bp
 * 8235: 8980: contig of 745 bp in length
 * 8981: 9080: gap of 100 bp
 * 9081: 9763: contig of 683 bp in length
 * 9764: 9863: gap of 100 bp

* 9864: 10479: contig of 616 bp in length
 * 10480: 10579: gap of 100 bp
 * 10580: 11203: contig of 624 bp in length
 * 11204: 11303: gap of 100 bp
 * 11304: 12043: contig of 740 bp in length
 * 12044: 12143: gap of 100 bp
 * 12144: 12846: contig of 703 bp in length
 * 12847: 12946: gap of 100 bp
 * 12947: 13478: contig of 732 bp in length
 * 13479: 13778: gap of 100 bp
 * 13779: 14542: contig of 764 bp in length
 * 14543: 14642: gap of 100 bp
 * 14643: 15366: contig of 724 bp in length
 * 15367: 15466: gap of 100 bp
 * 15467: 15160: contig of 694 bp in length
 * 16161: 16260: gap of 100 bp
 * 16261: 17005: contig of 805 bp in length
 * 17066: 17165: gap of 100 bp
 * 17166: 17914: contig of 749 bp in length
 * 17915: 18014: gap of 100 bp
 * 18015: 18715: contig of 701 bp in length
 * 18716: 18815: gap of 100 bp
 * 18816: 19416: contig of 621 bp in length
 * 19437: 19536: gap of 100 bp
 * 19537: 20176: contig of 640 bp in length
 * 20177: 20277: 2076: gap of 100 bp
 * 20277: 21013: contig of 737 bp in length
 * 21014: 21113: gap of 100 bp
 * 21114: 21872: contig of 759 bp in length
 * 2173: 21912: gap of 100 bp
 * 2197: 22635: 22734: gap of 100 bp
 * 22735: 22330: contig of 606 bp in length
 * 23341: 23440: 23441: 23441: 24159: contig of 719 bp in length
 * 23441: 24159: gap of 100 bp
 * 24160: 24259: gap of 100 bp
 * 24260: 24993: contig of 734 bp in length
 * 24994: 25093: gap of 100 bp
 * 25094: 25580: contig of 713 bp in length
 * 25807: 25906: gap of 100 bp
 * 25907: 26519: contig of 613 bp in length
 * 26520: 2669: gap of 100 bp
 * 26620: 27223: contig of 634 bp in length
 * 27254: 27353: gap of 100 bp
 * 27354: 28058: contig of 705 bp in length
 * 28059: 28158: gap of 100 bp
 * 28159: 28833: contig of 676 bp in length
 * 28835: 28944: gap of 100 bp
 * 28935: 29594: contig of 660 bp in length
 * 29595: 29694: gap of 100 bp
 * 29695: 30455: contig of 764 bp in length
 * 30459: 30556: gap of 100 bp
 * 30559: 31323: contig of 765 bp in length
 * 31324: 31433: gap of 100 bp
 * 31424: 32170: contig of 747 bp in length
 * 32171: 32270: gap of 100 bp
 * 32271: 33037: contig of 767 bp in length
 * 33038: 33137: gap of 100 bp
 * 33138: 33845: contig of 708 bp in length
 * 33846: 33945: gap of 100 bp
 * 33945: 34637: contig of 692 bp in length
 * 34638: 34737: gap of 100 bp
 * 34738: 35427: contig of 690 bp in length
 * 33428: 35527: gap of 100 bp
 * 35527: 36173: contig of 646 bp in length
 * 36174: 36223: gap of 100 bp
 * 36274: 366921: contig of 648 bp in length
 * 366921: 37021: gap of 100 bp
 * 37022: 37736: contig of 715 bp in length
 * 37737: 37836: gap of 100 bp
 * 37837: 38724: contig of 788 bp in length
 * 38725: 38724: gap of 100 bp
 * 38725: 39480: contig of 756 bp in length

reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

Quality of individual bases: this sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: http://gc.bcm.tmc.edu:8088/quality.info/genbank_annotation.html.

QUALSTAT-REPORT-----

Contig length: -----

Phrap values in estimate: -----

Average error rate (SCM-Phrap estimate): -----

Fraction of Phrap values less than 40 : -----

Number of consensus changing edits: -----

Number of N's in consensus :
62
61
62
63
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74
75
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77
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79
80
81
82
83

Contig length: -----

Phrap values in estimate: -----

Average error rate (SCM-Phrap estimate): -----

Fraction of Phrap values less than 40 : -----

Number of consensus changing edits: -----

Number of N's in consensus :
173652
170386
0.000194024
0.0280363
1401

Contig length: -----

Phrap values in estimate: -----

Average error rate (SCM-Phrap estimate): -----

Fraction of Phrap values less than 40 : -----

Number of consensus changing edits: -----

Number of N's in consensus :
17
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48

Contig length: -----

Phrap values in estimate: -----

Average error rate (SCM-Phrap estimate): -----

Fraction of Phrap values less than 40 : -----

Number of consensus changing edits: -----

Number of N's in consensus :
17
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----- Summary Statistics -----

Position	Original+Context	Edited+Context
1	...n(n)n(n)n(n)n(n)	...n(n)n(n)n(n)n(n)
2	...n(n)n(n)n(n)n(n)	...n(n)n(n)n(n)n(n)
3	...n(n)n(n)n(n)n(n)	...n(n)n(n)n(n)n(n)
4	...n(n)n(n)n(n)n(n)	...n(n)n(n)n(n)n(n)
5	...n(n)n(n)n(n)n(n)	...n(n)n(n)n(n)n(n)
6	...n(n)n(n)n(n)n(n)	...n(n)n(n)n(n)n(n)
7	...n(n)n(n)n(n)n(n)	...n(n)n(n)n(n)n(n)
8	...n(n)n(n)n(n)n(n)	...n(n)n(n)n(n)n(n)
9	...n(n)n(n)n(n)n(n)	...n(n)n(n)n(n)n(n)
10	...n(n)n(n)n(n)n(n)	...n(n)n(n)n(n)n(n)
11	...n(n)n(n)n(n)n(n)	...n(n)n(n)n(n)n(n)
12	...n(n)n(n)n(n)n(n)	...n(n)n(n)n(n)n(n)
13	...n(n)n(n)n(n)n(n)	...n(n)n(n)n(n)n(n)
14	...n(n)n(n)n(n)n(n)	...n(n)n(n)n(n)n(n)
15	...n(n)n(n)n(n)n(n)	...n(n)n(n)n(n)n(n)
16	...n(n)n(n)n(n)n(n)	...n(n)n(n)n(n)n(n)
17	...n(n)n(n)n(n)n(n)	...n(n)n(n)n(n)n(n)
18	...n(n)n(n)n(n)n(n)	...n(n)n(n)n(n)n(n)
19	...n(n)n(n)n(n)n(n)	...n(n)n(n)n(n)n(n)
20	...n(n)n(n)n(n)n(n)	...n(n)n(n)n(n)n(n)
21	...n(n)n(n)n(n)n(n)	...n(n)n(n)n(n)n(n)
22	...n(n)n(n)n(n)n(n)	...n(n)n(n)n(n)n(n)
23	...n(n)n(n)n(n)n(n)	...n(n)n(n)n(n)n(n)
24	...n(n)n(n)n(n)n(n)	...n(n)n(n)n(n)n(n)
25	...n(n)n(n)n(n)n(n)	...n(n)n(n)n(n)n(n)
26	...n(n)n(n)n(n)n(n)	...n(n)n(n)n(n)n(n)
27	...n(n)n(n)n(n)n(n)	...n(n)n(n)n(n)n(n)
28	...n(n)n(n)n(n)n(n)	...n(n)n(n)n(n)n(n)
29	...n(n)n(n)n(n)n(n)	...n(n)n(n)n(n)n(n)
30	...n(n)n(n)n(n)n(n)	...n(n)n(n)n(n)n(n)
31	...n(n)n(n)n(n)n(n)	...n(n)n(n)n(n)n(n)
32	...n(n)n(n)n(n)n(n)	...n(n)n(n)n(n)n(n)
33	...n(n)n(n)n(n)n(n)	...n(n)n(n)n(n)n(n)
34	...n(n)n(n)n(n)n(n)	...n(n)n(n)n(n)n(n)
35	...n(n)n(n)n(n)n(n)	...n(n)n(n)n(n)n(n)
36	...n(n)n(n)n(n)n(n)	...n(n)n(n)n(n)n(n)
37	...n(n)n(n)n(n)n(n)	...n(n)n(n)n(n)n(n)
38	...n(n)n(n)n(n)n(n)	...n(n)n(n)n(n)n(n)
39	...n(n)n(n)n(n)n(n)	...n(n)n(n)n(n)n(n)
40	...n(n)n(n)n(n)n(n)	...n(n)n(n)n(n)n(n)
41	...n(n)n(n)n(n)n(n)	...n(n)n(n)n(n)n(n)
42	...n(n)n(n)n(n)n(n)	...n(n)n(n)n(n)n(n)
43	...n(n)n(n)n(n)n(n)	...n(n)n(n)n(n)n(n)
44	...n(n)n(n)n(n)n(n)	...n(n)n(n)n(n)n(n)
45	...n(n)n(n)n(n)n(n)	...n(n)n(n)n(n)n(n)
46	...n(n)n(n)n(n)n(n)	...n(n)n(n)n(n)n(n)
47	...n(n)n(n)n(n)n(n)	...n(n)n(n)n(n)n(n)
48	...n(n)n(n)n(n)n(n)	...n(n)n(n)n(n)n(n)

----- Consensus changing edits -----

Position	Original+Context	Edited+Context
1	...n(n)n(n)n(n)n(n)	...n(n)n(n)n(n)n(n)
2	...n(n)n(n)n(n)n(n)	...n(n)n(n)n(n)n(n)
3	...n(n)n(n)n(n)n(n)	...n(n)n(n)n(n)n(n)
4	...n(n)n(n)n(n)n(n)	...n(n)n(n)n(n)n(n)
5	...n(n)n(n)n(n)n(n)	...n(n)n(n)n(n)n(n)
6	...n(n)n(n)n(n)n(n)	...n(n)n(n)n(n)n(n)
7	...n(n)n(n)n(n)n(n)	...n(n)n(n)n(n)n(n)
8	...n(n)n(n)n(n)n(n)	...n(n)n(n)n(n)n(n)
9	...n(n)n(n)n(n)n(n)	...n(n)n(n)n(n)n(n)
10	...n(n)n(n)n(n)n(n)	...n(n)n(n)n(n)n(n)
11	...n(n)n(n)n(n)n(n)	...n(n)n(n)n(n)n(n)
12	...n(n)n(n)n(n)n(n)	...n(n)n(n)n(n)n(n)
13	...n(n)n(n)n(n)n(n)	...n(n)n(n)n(n)n(n)
14	...n(n)n(n)n(n)n(n)	...n(n)n(n)n(n)n(n)
15	...n(n)n(n)n(n)n(n)	...n(n)n(n)n(n)n(n)
16	...n(n)n(n)n(n)n(n)	...n(n)n(n)n(n)n(n)
17	...n(n)n(n)n(n)n(n)	...n(n)n(n)n(n)n(n)
18	...n(n)n(n)n(n)n(n)	...n(n)n(n)n(n)n(n)
19	...n(n)n(n)n(n)n(n)	...n(n)n(n)n(n)n(n)
20	...n(n)n(n)n(n)n(n)	...n(n)n(n)n(n)n(n)
21	...n(n)n(n)n(n)n(n)	...n(n)n(n)n(n)n(n)
22	...n(n)n(n)n(n)n(n)	...n(n)n(n)n(n)n(n)
23	...n(n)n(n)n(n)n(n)	...n(n)n(n)n(n)n(n)
24	...n(n)n(n)n(n)n(n)	...n(n)n(n)n(n)n(n)
25	...n(n)n(n)n(n)n(n)	...n(n)n(n)n(n)n(n)
26	...n(n)n(n)n(n)n(n)	...n(n)n(n)n(n)n(n)
27	...n(n)n(n)n(n)n(n)	...n(n)n(n)n(n)n(n)
28	...n(n)n(n)n(n)n(n)	...n(n)n(n)n(n)n(n)
29	...n(n)n(n)n(n)n(n)	...n(n)n(n)n(n)n(n)
30	...n(n)n(n)n(n)n(n)	...n(n)n(n)n(n)n(n)
31	...n(n)n(n)n(n)n(n)	...n(n)n(n)n(n)n(n)
32	...n(n)n(n)n(n)n(n)	...n(n)n(n)n(n)n(n)
33	...n(n)n(n)n(n)n(n)	...n(n)n(n)n(n)n(n)
34	...n(n)n(n)n(n)n(n)	...n(n)n(n)n(n)n(n)
35	...n(n)n(n)n(n)n(n)	...n(n)n(n)n(n)n(n)
36	...n(n)n(n)n(n)n(n)	...n(n)n(n)n(n)n(n)
37	...n(n)n(n)n(n)n(n)	...n(n)n(n)n(n)n(n)
38	...n(n)n(n)n(n)n(n)	...n(n)n(n)n(n)n(n)
39	...n(n)n(n)n(n)n(n)	...n(n)n(n)n(n)n(n)
40	...n(n)n(n)n(n)n(n)	...n(n)n(n)n(n)n(n)
41	...n(n)n(n)n(n)n(n)	...n(n)n(n)n(n)n(n)
42	...n(n)n(n)n(n)n(n)	...n(n)n(n)n(n)n(n)
43	...n(n)n(n)n(n)n(n)	...n(n)n(n)n(n)n(n)
44	...n(n)n(n)n(n)n(n)	...n(n)n(n)n(n)n(n)
45	...n(n)n(n)n(n)n(n)	...n(n)n(n)n(n)n(n)
46	...n(n)n(n)n(n)n(n)	...n(n)n(n)n(n)n(n)
47	...n(n)n(n)n(n)n(n)	...n(n)n(n)n(n)n(n)
48	...n(n)n(n)n(n)n(n)	...n(n)n(n)n(n)n(n)

Query Match Best Local Similarity 90.6%; Score 15,4; DB 88; Job time: 2709 sec

QY 1 TTYGARGARATGGAYCC 17

Db 69860 TTYGAGAGATGGATCC 69844

Search completed: May 14, 2001, 19:10:01

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model.

Run on: May 15, 2001, 10:13:29 ; Search time 1105.85 Seconds

(without alignments)
226.716 Million cell updates/sec

Title: US-09-373-230-5
Perfect score: 17
Sequence: 1 TTYGARGARATGGAYCC 17
Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 1283235 seqs, 7373929652 residues
Total number of hits satisfying chosen parameters: 2566470
Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*

1: gb_ba1:*

2: gb_ba2:*

3: gb_ba3:*

4: gb_in1:*

5: gb_in2:*

6: gb_in3:*

7: gb_om:*

8: gb_ov:*

9: gb_pati:*

10: gb_pst2:*

11: gb_ph:*

12: gb_p11:*

13: gb_p12:*

14: gb_p13:*

15: gb_p14:*

16: em_ba1:*

17: em_ba2:*

18: em_fun:*

19: em_htco_hun:*

20: em_higo_inv:*

21: em_higo_rid:*

22: em_htq_hum1:*

23: em_htq_hum2:*

24: em_htq_hum3:*

25: em_htq_hum4:*

26: em_hig_hum5:*

27: em_hig_hum6:*

28: em_hig_hum7:*

29: em_hig_hum8:*

30: em_hig_inv1:*

31: em_htq_inv2:*

32: em_htq_other:*

33: em_hig_rid:*

34: em_hum1:*

35: em_hum2:*

36: em_hum3:*

37: em_hum4:*

38: em_hum5:*

39: em_hum6:*

40: em_hum7:*

41: em_in:*

42: em_on:*

43: em_or:*

44: em_ov:*

45: em_pat:*

46: em_ph:*

47: em_D1:*

48: em_ro:*

49: em_sts:*

50: em_sy:*

51: em_un:*

52: em_v1:*

53: gb_sts1:*

54: gb_sts2:*

55: gb_sts3:*

56: gb_sy:*

57: gb_un:*

58: gb_v1:*

59: gb_v12:*

60: gb_htg1:*

61: gb_htg2:*

62: gb_htg3:*

63: gb_htg4:*

64: gb_htg5:*

65: gb_htg6:*

66: gb_htg7:*

67: gb_htg8:*

68: gb_htg9:*

69: gb_htg10:*

70: gb_htg11:*

71: gb_htg12:*

72: gb_htg13:*

73: gb_htg14:*

74: gb_htg15:*

75: gb_htg16:*

76: gb_htg17:*

77: gb_htg18:*

78: gb_htg19:*

79: gb_htg20:*

80: gb_htg21:*

81: gb_htg22:*

82: gb_htg23:*

83: gb_htg24:*

84: gb_htg25:*

85: gb_pr1:*

86: gb_pr2:*

87: gb_pr3:*

88: gb_pr4:*

89: gb_pr5:*

90: gb_pr6:*

91: gb_pr7:*

92: gb_pr8:*

93: gb_pr9:*

94: gb_r01:*

95: gb_r02:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB ID	Description
1	15.4	90.6	17	9 AR072047	AR072047 Sequence
2	15.4	90.6	471	9 AR072044	AR072044 Sequence
3	15.4	90.6	471	10 E13264	E13264 Mouse cDNA
4	15.4	90.6	471	10 E14257	E14257 cDNA encodi
5	15.4	90.6	471	10 E14760	E14760 cDNA encodi
6	15.4	90.6	471	10 E17139	E17139 Murine mRNA
7	15.4	90.6	471	45 E10609	E10609 Mouse cDNA
8	15.4	90.6	471	45 E11744	E11744 cDNA encodi
9	15.4	90.6	471	45 E12010	E12010 cDNA encodi
10	15.4	90.6	471	56 ASIGIF	Y09278 Artificial
11	15.4	90.6	572	94 MMU66244	U66244 Mus musculu

ORIGIN

Query Match 90.6%; Score 15.4; DB 10; Length 471;
 Best Local Similarity 76.5%; Pred. No. 4.5e+02;
 Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTYGARGARATGGAYCC 17
 ||:||:||:||:||:||:||:
 Db 244 TTGAGGAATGGATCC 260

RESULT 4

ORGANISM Mus sp.

REFERENCE 1 (bases 1 to 471);
 AUTHORS Ushio,S., Torisoe,K., Tanimoto,T., Okamura,H. and Kurimoto,M.
 TITLE POLYPEPTIDE INDUCING PRODUCTION OF INTERFERON-GAMMA
 JOURNAL PATENT: JP 199807659-A 2 13 JAN-1998;
 HAYASHIBARA BIOCHEM LAB INC

COMMENT

ACCESSION E14760
 VERSION E14760.1 GI:5709443
 KEYWORDS JP 199807659-A/2.
 SOURCE Mus sp.

REFERENCE 1 (bases 1 to 471);
 AUTHORS Ushio,S., Torisoe,K., Tanimoto,T., Okamura,H. and Kurimoto,M.
 TITLE POLYPEPTIDE INDUCING PRODUCTION OF INTERFERON-GAMMA
 JOURNAL PATENT: JP 199807659-A 2 13 JAN-1998;
 HAYASHIBARA BIOCHEM LAB INC

COMMENT

ACCESSION E14257
 VERSION E14257
 DEFINITION cDNA encoding mouse interferon gamma-inducing factor.
 ACCESSION E14257
 VERSION E14257.1 GI:5708940
 KEYWORDS JPN 1997289896-A/1.

ORGANISM Mus sp.

REFERENCE 1 (bases 1 to 471);
 AUTHORS Akita,K., Nukada,Y., Fujii,M., Tanimoto,T. and Kurimoto,M.
 TITLE PROTEIN FOR INDUCING PRODUCTION OF INTERFERON-GAMMA IN IMMUNOCOMPETENT CELL
 JOURNAL Patent: JP 1997289896-A 1 11-NOV-1997;
 HAYASHIBARA BIOCHEM LAB INC

COMMENT

OS Mus sp. (mouse)
 PN JP 1997289896-A/1

PF 26-SEP-1995 JP 1996269105
 PR 27/07/25, 29-FEB-1996 JP 96P 67434 PI
 AKITA, KENJI, NUKADA, YOSHIVIKI, FUJII, MITSUKIYO, TANIMOTO, TABAO, PI
 KURIMOTO, MASASHI
 PC C12P21/02, A61K9/06, A61K38/00, A61K38/00, A61K38/00, PC

PC A61K38/00, A61K38/00, C07K14/47, (C12P21/02, C12R1:91); CC
 strandedness: double;
 CC topology: Linear;
 CC hypothetical: No;
 CC anti-sense: No;
 FH Key
 FT source 1. .471
 /organism='Mus sp.'
 /tissue_type='liver'
 /db_xref='taxon:10095'
 /product='mouse interferon gamma-inducing factor'
 FT mat_peptide
 FT source 1. .471
 /organism='Mus sp.'
 /tissue_type='liver'
 /db_xref='taxon:10095'
 FEATURES source
 BASE COUNT 162 a 91 c 92 g 125 t 1 others

RESULT 6

ORGANISM Mus sp.

REFERENCE 1 (bases 1 to 471);
 AUTHORS Matthew,T.G., Nicholl,J.H., Udagawa,N. and Kurimoto,M.
 TITLE OSTEOCLAST-FORMATION INHIBITOR
 JOURNAL Patent: JP 1998236974-A 5 08-SEP-1998;
 HAYASHIBARA BIOCHEM LAB INC

COMMENT

ACCESSION E17139
 VERSION E17139
 DEFINITION Murine mRNA for interleukin-18 (IL-18). PAT 28-JUL-1999
 KEYWORDS JPN 1998236974-A/5.

ORGANISM Mus sp.

REFERENCE 1 (bases 1 to 471);
 AUTHORS Matthew,T.G., Nicholl,J.H., Udagawa,N. and Kurimoto,M.
 TITLE OSTEOCLAST-FORMATION INHIBITOR
 JOURNAL Patent: JP 1998236974-A 5 08-SEP-1998;
 HAYASHIBARA BIOCHEM LAB INC

COMMENT

ACCESSION E14760
 VERSION E14760
 DEFINITION cDNA encoding polypeptide which induces interferon-gamma production HIGF.

RESULT 5

ACCESSION E14760
 VERSION E14760
 DEFINITION cDNA encoding polypeptide which induces interferon-gamma production HIGF.

QY 1 TTYGARGARATGGAYCC 17
 ||:||:||:||:||:||:||:||:
 Db 244 TTGAGGAATGGATCC 260

RESULT 9
 E12010 ID E12010 standard; RNA; ROD; 471 BP.
 XX AC E12010;
 XX SV E12010.1
 XX DT 07-OCT-1997 (Rel. 52, Created)
 DT 02-SEP-2000 (Rel. 65, last updated, version 2)
 XX DE cDNA encoding mouse polypeptide which introduce interferon-gamma product in immunocompetent cell.
 XX DE DE immunocompetent cell.
 KW XX JP 1996231598-A/2.

OS Mus musculus (house mouse)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
 OC Muridae; Murinae; Mus.
 RN [1]
 RP 1-471
 RA Kunioka T., Taniguchi M., Kono K., Kurimoto M.;
 RT "MONOCLONAL ANTIBODY";
 RL Patent number JP1996231598-A/2, 10-SEP-1996.
 RL HAYASHIBARA BIOCHEM LAB INC.
 XX OS Mus musculus (mouse)
 CC PN JP 1996231598-A/2
 CC PD 10-SEP-1996
 CC PF 23-FEB-1995 JP 1995058240
 CC PI KUNIKATA TOSHIRO, TANIGUCHI MITSUKO, KONO KEIZO,
 CC PT KURIKOMOTO MASASHI
 CC PC C07K1/67/24, C07K1/16, C07K1/18, C07K1/22, C07K1/26, C07K1/30,
 CC PC C12N15/02, C12P21/08, G01N33/57//A61K38/21, A61K39/395,
 CC PC (C12P21/08,
 CC PC C12R1/91);
 CC CC strandness: Double;
 CC CC topology: Linear;
 CC CC hypothetical: No;
 CC CC anti-sense: No;
 CC CC Key
 CC FH Location/Qualifiers
 CC FT source 1. .471
 CC CC 1. .471
 CC CC /organism="Mus musculus"
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 XX FH Key
 FH Location/Qualifiers
 FT source 1. .471
 FT /db_xref="taxon:10090"
 FT /organism="Mus musculus"
 XX SQ Sequence 471 BP; 162 A; 91 C; 92 G; 125 T; 1 other;

Query Match 90.6%; Score 15.4; DB 45; Length 471;
 Best Local Similarity 76.5%; Pred. No. 4.5e+02;
 Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 Version U66244.1 GI:1561735

RESULT 11
 MMU6244 LOCUS MMU6244 572 bp_rna mRNA, partial cds.
 DEFINITION Mus musculus interferon-gamma inducing factor mRNA, partial cds.
 ACCESSION U66244
 VERSION U66244.1
 KEYWORDS house mouse.
 SOURCE
 ORGANISM Mus musculus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 572)
 AUTHORS Rothe,H., Jenkins,N.A., Copeland,N.G. and Kolb,H.
 TITLE Active stage of autoimmune diabetes is associated with the expression of a novel cytokine, Igf, which is located near Idd2
 JOURNAL J. Clin. Invest. 99 (3), 469-474 (1997)
 MEDLINE 97174346
 REFERENCE 2 (bases 1 to 572)
 AUTHORS Rothe,H., Copeland,N.G. and Kolb,H.
 TITLE Direct Submission
 JOURNAL Submitted (06 AUG-1996) Diabetes Research Institute, Auf'm Hennekamp 65, Dueseldorf 40225, Germany
 FEATURES location/Qualifiers
 SOURCE 1. .572
 /organism="Mus musculus"
 /strain="non obese diabetic (NOD)"
 /db_xref="taxon:10090"
 /chromosome="9"
 /tissue_type="pancreas"

Query Match 90.6%; Score 15.4; DB 45; Length 471;
 Best Local Similarity 76.5%; Pred. No. 4.5e+02;
 Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TTYGARGARATGGAYCC 17
 QY ||:||:||:||:||:||:
 Db 244 TTGAGGAATGGATCC 260

RESULT 10

TITLE	Homo sapiens chromosome 4, clone CTD-2353K2
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 59955)
AUTHORS	Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Barna, N., Bastien, V., Beda, F., Bousliskiy, L., Boukhalfa, B., Brown, A., Chaoel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Hartford, A., Horton, L., Ilev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., LaCroix, K., Lamazares, R., Landers, T., Lehocky, J., Levine, R., Lieu, C., Liu, G., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McKernan, K., McPheeeters, R., Melton, J., Meneis, L., Minova, T., Mlenga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, T.M., Oliver, J., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Rieback, M., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, C., Severy, P., Sougnez, C., Spencer, B., Strange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talanias, V., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J., Vasilev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zimmer, A., and Zody, M.
COMMENT	Submitted (23-SEP-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
JOURNAL	Center: Whitehead Institute/ MIT Center for Genome Research Center code: WBR Web site: http://www-seq.wi.mit.edu Contact: sequence_submissions@genome.wi.mit.edu Project Information Center project name: LI0743 Center clone name: 2353_K_2
NOTE:	This record contains 74 individual sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will be preserved.
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*	646 745: gap of 100 bp
*	746 1464: contig of 719 bp in length
*	1465 1564: gap of 100 bp
*	1565 2315: contig of 751 bp in length
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*	2416 3059: contig of 664 bp in length
*	3060 3159: gap of 100 bp
*	3160 3877: contig of 718 bp in length
*	3878 3977: gap of 100 bp
*	3978 4722: contig of 745 bp in length
*	4723 4822: gap of 100 bp
*	4823 5579: contig of 754 bp in length
*	5580 5679: gap of 100 bp
*	5680 6315: contig of 636 bp in length
*	6316 6415: gap of 100 bp
*	6416 7280: contig of 865 bp in length
*	7281 7380: gap of 100 bp
*	7381 8134: contig of 754 bp in length
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*	9864 10479: contig of 616 bp in length
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*	11204 11303: gap of 100 bp
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*	12044 12143: gap of 100 bp
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*	13679 13778: gap of 100 bp
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*	16261 17065: contig of 805 bp in length
*	17066 17765: gap of 100 bp
*	17166 17914: contig of 749 bp in length
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*	21973 22633: contig of 662 bp in length
*	22635 22734: gap of 100 bp
*	22735 22340: contig of 606 bp in length
*	22735 22734: gap of 100 bp
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*	28059 28158: gap of 100 bp
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*	30459 30558: gap of 100 bp
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*	32171 32270: gap of 100 bp
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*	33038 33137: gap of 100 bp
*	33138 33845: contig of 708 bp in length
*	33846 33945: gap of 100 bp
*	33946 34637: contig of 692 bp in length
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*	36174 36273: gap of 100 bp
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*	36922 37021: gap of 100 bp
*	37022 37736: contig of 715 bp in length
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39481	39580:	gap of 100 bp				Davy-Carroll,L., Dederon,D.A., Deane,K.K., Delgado,J.,
39581	40327:	contig of 747 bp in length				Denn,A.L., Ding,Y., Dinh,H.B., Doughwaite,M.J., Draper,H.,
40328	40427:	gap of 100 bp				Dugan-Rocha,S., Durbin,K.J., Eberhardt,C., Edgar,D., Edwards,C.C.,
40428	41108:	contig of 761 bp in length				Elli,J.C., Emelting,S., Escott,M., Failes,T., Ferrarauto,D.,
41189	41288:	gap of 100 bp				Flaagg,N.J., Ford,J.J., Foster,P., Frantz,J., Gabisi,A., Gao,J.,
41289	42060:	contig of 772 bp in length				Garcia,A., Garner,T., Garza,N., Gill,R., Gorelli,J.H., Guevara,W.,
42161	42160:	gap of 100 bp				Gunaratne,P., Hale,S., Hamilton,K., Han,J., Harris,C.,
42161	42894:	contig of 734 bp in length				Hart,M., Havlik,P., Hawes,A., Hernandez,J., Hernandez,O.,
42895	42954:	gap of 100 bp				Hodgson,A., Hoopes,M., Holloway,C., Hollins,B., Homsi,F., Jackson,L.E.,
42995	43747:	contig of 753 bp in length				Howards,S., Huber,J., Hulyk,S., Hume,J., Ioshikhes,I., Jackson,L.E.,
43748	43847:	gap of 100 bp				Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Jordan,S., Koval,C.,
43848	44463:	contig of 615 bp in length				Karlsson,E., Kelly,S., Khan,U., King,B., Kovari,C.,
44692	44991:	gap of 100 bp				Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lee,L.C.,
44693	45452:	contig of 706 bp in length				Lewis,L., Li,J., Li,Z., Lichatowicz,C., Lieu,C., Liu,J., Liu,W.,
44693	45191:	contig of 635 bp in length				Louiseed,H., Lozada,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R.,
45198	45297:	gap of 100 bp				Ma,J., Maheshwari,M., Mapua,P., Marcondel,I., Martin,R., McLeod,M.P.,
45298	46044:	contig of 737 bp in length				Martinale,A., Martinez,E., Mawhinney,E., McLeod,M.P.,
46135	46134:	contig of 641 bp in length				Medor,M., Meller,G., Mercher,S., Metzker,M., Miller,A., Miner,G.,
46892	46991:	gap of 100 bp				Miller,Z., Mitchell,T., Mohabbat,N., Montgomery,K.T., Morgan,M.,
46992	47697:	contig of 706 bp in length				Morris,S., Moser,M., Neal,D., Nelson,D., Newton,J., Newton,N.,
47698	47797:	gap of 100 bp				Nguyen,A., Nguyen,N., Nguyen,N., Nickerson,B., Nwokekwu,S.,
47798	48532:	contig of 755 bp in length				Oguri,M., Okwunuo,G., Oragunye,A., Oviido,R., Payton,B.,
48553	48652:	gap of 100 bp				Perry,J., Perez,L., Peters,L., Pickens,R., Primis,E., Pu,L.L.,
48653	49293:	contig of 641 bp in length				Quille,M., Reyz,Y., Rives,M., Rojas,A., Rojubopakorn,I., Roife,M.,
49294	49393:	gap of 100 bp				Ruitz,S., Savery,G., Scherer,S., Scott,G., Shen,H., Shim,C.,
49394	50099:	contig of 706 bp in length				Shooshtari,N., Sisson,L., Sodergreen,B., Sonike,T., Sparks,A.,
50101	50199:	gap of 100 bp				Stanley,H., Stone,H., Sutton,J., Svatek,A., Tabor,P., Tammerisa,A.,
50200	50957:	contig of 758 bp in length				Tamerisa,K., Tang,H., Tansey,J., Taylor,C., Taylor,T., Telfrord,B.,
50958	51057:	gap of 100 bp				Thomas,N., Thomas,S., Usmani,L., Vasquez,L., Vela,V., Villalon,D.,
51058	51840:	contig of 783 bp in length				Vinson,R., Wall,R., Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S., Williams,G., Williamson,A.,
51841	51940:	gap of 100 bp				Wleczky,R., Wooden,S., Worley,K., Wu,C., Wu,Y.F., Wu,Y., Zhou,J.,
52064	52645:	contig of 705 bp in length				Zorrilla,S., Kucherlapati,R. and Gibbs,R.
52646	52745:	gap of 100 bp				
52746	53371:	contig of 626 bp in length				
53372	53471:	gap of 100 bp				
53472	54088:	contig of 617 bp in length				
54089	54188:	gap of 100 bp				
54189	54963:	contig of 775 bp in length				
54964	55063:	gap of 100 bp				
55064	55797:	contig of 734 bp in length				
55798	55897:	gap of 100 bp				
55898	56622:	contig of 725 bp in length				
Query Match	90.6%;	DB 77; Length 5995;				
Best Local Similarity	76.7%;	PScore: No. 6.8e+02;				
Matches	13;	Conservative 4;	Mismatches 0;	Indels 0;	Gaps 0;	
1	TTYGARGARGATGGAYC	17				
55674	TTTGAGAAGATGGGCC	55690				
REFERENCE	JOURNAL					
AUTHORS						
TITLE						
JOURNAL						
COMMENT						
INFORMATION:						
9C-HELP@BCBM.TMC.EDU						
CLONE LENGTH:						
entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the features listing.						
ANNOTATION OF FEATURES:						
SRSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.						
Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished) for Human and Mouse sequences.						
Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.						
SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2						

reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: this sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: <http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html>.

QUALSTAR-REPORT-----

----- Summary Statistics -----

Contig length:

173652

Phrap values in estimate:

170386

Average error rate (BCM-Phrap estimate):

0.000194024

Fraction of Phrap values less than 40 :

0.0280363

Number of consensus changing edits:

1401

Number of N's in consensus : 0

----- Consensus changing edits -----

Position Original+Context Edited+Context

1(n)nnnnnnn(t)aaagt
2(n)nnnnnnn(t)(a)gggtgc
3(n)nnnnnnn(ta)(g)ttgtggaa
4(n)nnnnnnn(tag)(t)tgcaaggaa
5(n)nnnnnnn(tag(t))ttcaaggac
6(n)nnnnnnn(tag(t))ttcaaggac
7(n)nnnnnnn(tag(t))ttcaaggac
8(n)nnnnnnn(tag(t))ttcaaggac
9(n)nnnnnnn(tag(t))ttcaaggac
10(n)nnnnnnn(tag(t))ttcaaggac
11	nnnnnnnn(n)nnnnnnn	tttgttccaa(g)gaacngatac
12	nnnnnnnn(n)nnnnnnn	aggtttgcag(j)aacatcttca
13	nnnnnnnn(n)nnnnnnn	gttgttcagg(j)aacatcttca
14	nnnnnnnn(n)nnnnnnn	gttgttcagg(j)aacatcttca
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17	nnnnnnnn(n)nnnnnnn	gttgttcagg(j)aacatcttca
18	nnnnnnnn(n)nnnnnnn	gttgttcagg(j)aacatcttca
19	nnnnnnnn(n)nnnnnnn	gttgttcagg(j)aacatcttca
20	nnnnnnnn(n)nnnnnnn	gttgttcagg(j)aacatcttca
21	nnnnnnnn(n)nnnnnnn	gttgttcagg(j)aacatcttca
22	nnnnnnnn(n)nnnnnnn	gttgttcagg(j)aacatcttca
23	nnnnnnnn(n)nnnnnnn	gttgttcagg(j)aacatcttca
24	nnnnnnnn(n)nnnnnnn	gttgttcagg(j)aacatcttca
25	nnnnnnnn(n)nnnnnnn	gttgttcagg(j)aacatcttca
26	nnnnnnnn(n)nnnnnnn	gttgttcagg(j)aacatcttca
27	nnnnnnnn(n)nnnnnnn	gttgttcagg(j)aacatcttca
28	nnnnnnnn(n)nnnnnnn	gttgttcagg(j)aacatcttca
29	nnnnnnnn(n)nnnnnnn	gttgttcagg(j)aacatcttca
30	nnnnnnnn(n)nnnnnnn	gttgttcagg(j)aacatcttca
31	nnnnnnnn(n)nnnnnnn	gttgttcagg(j)aacatcttca
32	nnnnnnnn(n)nnnnnnn	gttgttcagg(j)aacatcttca
33	nnnnnnnn(n)nnnnnnn	gttgttcagg(j)aacatcttca
34	nnnnnnnn(n)nnnnnnn	gttgttcagg(j)aacatcttca
35	nnnnnnnn(n)nnnnnnn	gttgttcagg(j)aacatcttca
36	nnnnnnnn(n)nnnnnnn	gttgttcagg(j)aacatcttca
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38	nnnnnnnn(n)nnnnnnn	gttgttcagg(j)aacatcttca
39	nnnnnnnn(n)nnnnnnn	gttgttcagg(j)aacatcttca
40	nnnnnnnn(n)nnnnnnn	gttgttcagg(j)aacatcttca
41	nnnnnnnn(n)nnnnnnn	gttgttcagg(j)aacatcttca
42	nnnnnnnn(n)nnnnnnn	gttgttcagg(j)aacatcttca
43	nnnnnnnn(n)nnnnnnn	gttgttcagg(j)aacatcttca
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----- Query Match -----

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RESULT 16 AP000144/C

DEFINITION AP000144

LOCUS 100000 bp DNA

DEFINITION Homo sapiens genomic DNA, chromosome 21q21.2, LL56-APP region, clone B291C14-R4F3, segment 9/10, complete sequence.

ACCESSION AP000144

VERSION AP000144.1

KEYWORDS GI:4827110

HGT.

SOURCE

ORGANISM Homo sapiens DNA.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 100000)

AUTHORS Hattori, M., Ishii, K., Toyoda, A., Taylor, T.D., Hong-Seq, P., Fujiyama, A., Yada, T., Totoki, Y. and Sasaki, Y.

TITLE HOMO sapiens 911,949bp genomic DNA of 21q21.2 (REGION: LL56-APP CLONE RANGE: B291C14-R4F3)

JOURNAL Published Only in DataBase (1999) In press

2 (bases 1 to 100000)

REFERENCE

AUTHORS Hattori, M., Ishii, K., Toyoda, A., Taylor, T.D., Hong-Seq, P., Fujiyama, A., Yada, T., Totoki, Y. and Sasaki, Y.

TITLE Direct Submission

JOURNAL Submitted (10-MAY-1999) to the DDBJ/EMBL/GenBank databases.

Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555, Japan

(E-mail:hattori@gsc.riken.go.jp, URL:<http://hgp-gsc.riken.go.jp/>, Tel:81-42-778-9923, Fax:81-42-778-9924)

VERSION	AC010176.12	GI	10190751
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SOURCE	Human.	SEARCHES	searches
ORGANISM	Homo sapiens	FROM	dbSTS, GDB, and
REFERENCE	1 (bases 1 to 202103)	TO	local mapping efforts.
AUTHORS	Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C., Alisbrooks, S.L., Amaralunge, H.C., Are, J.R., Banks, T., Barbaria, J., Bentzon, J.J., Binage, K., Blankenburg, K., Bonin, D., Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buahy, C., Burch, P., Burkhardt, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chiu, D., Choudhury, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davis, M.L., Davis, C., Davy-Carroll, L., Bedrich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dunn-Rocha, S., Durbin, K.J., Earhart, C., Edgar, D., Edwards, C.C., Elhaij, C., Emerling, S., Escott, M., Fallis, T., Ferrautio, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Guarante, P., Hale, S., Hamilton, K., Han, J., Harris, C., Harris, K., Hart, M., Havlak, P., Hayes, R., Hernandez, J., Hernandez, O., Hodgson, A., Hoque, M., Hollaway, C., Hollins, B., Homsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Iochikies, T., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudan, S., Karlsson, E., Kelly, S., Khan, U., King, L., Kovach, J., Kovar, C., Katoricci, J., Kurek, A., Landry, N., Leel, B., Lee, E., Lewis, L.C., Lewis, L., Li, J., Li, Z., Lichter, O., Lieu, C., Liu, J., Liu, W., Louisberg, H., Lozada, R., Lu, X., Lucier, A., Lucier, R., Luna, R., Martindale, A., Martinez, E., Massey, E., Mawliney, E., McLeod, M.P., Meadow, M., Meli, G., Merscher, S., Metzker, M., Miller, A., Miner, G., Miner, Z., Mitchell, J., Mohabbat, K., Montgomery, R.T., Morgan, M., Morris, S., Moser, M., Neal, D., Nelson, D., Newtonson, J., Newtonson, N., Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nwolekwo, S., Oguri, M., Okwuonu, G., Oragunye, N., Oriodo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L., Quilles, M., Ren, Y., Rives, M., Rojibokan, I., Roiffe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shim, C., Shoopstari, N., Sisson, P., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Stratek, P., Tamervisa, A., Tamervisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Villalon, D., Washington, R., Wall, R., Wang, S., Ward-Moore, S., Warren, R.,' Wleczek, R., Woods, S., Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Kucherlapati, R., and Gibbs, R.	REPEATS	Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.
REFERENCE	2 (bases 1 to 202103)	GENE	Genes and region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (<math>\text{expect} < 1e-34</math>) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.
AUTHORS	Worley, K.C.	SEQUENCING READ COVERAGE	sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.
JOURNAL	Direct Submission	QUALITY OF INDIVIDUAL BASES	This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: http://gc.bom.tmc.edu:8088/quality.info/genbank.annotation.html .
REFERENCE	3 (bases 1 to 202103)	PHIPAP VALUES	Phipap values in estimate: Average error rate (BCM-Phipap estimate): 9.7754e-05 Fraction of Phipap values less than 40%: 0.0287005 Number of consensus changing edits: 29 Number of N's in consensus : 0
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JOURNAL	Direct Submission	-----	-----
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/rpt_family="LINE/L1"
/rpt_type=DISPERSED

repeat_region          STS
repeat_region          /rpt_type=DISPERSED
repeat_region          13676..13790
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/note="AFMa556z19"
/DB_XREF="GDB:9132389"
/ACCESSION_NO. M3112"
repeat_region          complement(1347..14027)
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/rpt_family="SINE/Alu"
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repeat_region          14028..14430
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repeat_region          14431..14742
/note="AlusX"
/rpt_family="SINE/Alu"
/rpt_type=DISPERSED
repeat_region          14743..14806
/note="LIM4"
/rpt_family="LINE/L1"
/rpt_type=DISPERSED
repeat_region          15768..16072
/note="AlusX"
/rpt_family="SINE/Alu"
/rpt_type=DISPERSED
repeat_region          17881..18012
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/rpt_type=DISPERSED
repeat_region          complement(18041..18207)
/note="MER91A"
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repeat_region          complement(18416..18684)
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/rpt_family="SINE/Alu"
/rpt_type=DISPERSED
repeat_region          complement(18982..19899)
/note="LIMC5"
/rpt_family="LINE/L1"
/rpt_type=DISPERSED
repeat_region          20230..20272
/note="n.(CA)n"

Query Match          90.6%; Score 15.4; DB 90; Length 340000;
repeat_region          Best Local Similarity 76.5%; Pred. No. 7.8e+02;
repeat_region          Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
repeat_region          QY          1 TTIGGARRGATGGAYCC 17
repeat_region          Db 273372 TTTGAGGAAATGATC 273356

RESULT              21
G01707               Locus          G01707          355 bp       DNA
DEFINITION           Definition      chicken STS ADI288.          STS
ACCESSION            Accession      G01707
VERSION              Version        G01707.1 GI:559231
KEYWORDS             Keywords       STS sequence; primer; sequence tagged site.
SOURCE               Source         chicken vector-pBluescript II RS+ host-E. coli.
ORGANISM             Organism      Gallus gallus
Eukaryota; Miochondria; Metazoa; Chordata; Vertebrata; Tetrapoda;
Aves; Neognathae; Galliformes; Phasianidae; Phasianine; Gallus.
REFERENCE            Reference     1 (bases 1 to 355)
AUTHORS              Authors        Cheng, H.H.
JOURNAL              Journal       Unpublished (1994)
COMMENT              Comment      Synonyms: B407
Contact: Hans H. Cheng
Avian Disease and Oncology Laboratory
USDA-ARS
3606 E. Mount Hope Rd, East Lansing, MI 48823, USA
Tel: 5173376758

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Fax: 5173376776
Email: hccheng@pilot.msu.edu

Primer A: AAACTTGCTCCAACTT
Primer B: ATCCCCACGTAACTTAT
STS size: 152

PCR profile:
Denaturation: 94 degrees C for 1 minute
Annealing: 48 degrees C for 1 minute
Polymerization: 72 degrees C for 1 minute

Thermal Cycler: MJ Research

Protocol:
Template: 50-100 ng
Primer: 0.1 uM
dNTPs: 200 uM
Tag polymerase: 0.4 units/uL
Total Vol: 25 uL

Buffer:
MgCl2: 1.5 mM
KCl: 50 mM
TRIS-HCl: 10 mM
PH: 9.0
Triton X-100: 0.1 %.

FEATURES
source
ST5
primer_bind
primer_bind complement(334..353)
BASE COUNT 75 a 69 c 86 g 124 t 1 others
ORIGIN

Query Match 84.7%; Score 14.4; DB 54; Length 355;
Best Local Similarity 75.0%; Pred. No. 1.7e+03; Mismatches 0;
Matches 12; Conservativity 4; Indels 0; Gaps 0;

QY ||:||:||:||:||:||:
Db 301 TTGAGGAATGGTC 316

RESULT 22
MMHBEGFL4
LOCUS MMHBEGFL4 710 bp DNA
DEFINITION MUS musculus heparin-binding epidermal growth factor-like growth factor gene, exon 5 and 6, complete cds.
ACCESSION U31912
VERSION U31912.1
KEYWORDS G1:1236398
SEGMENT 4 of 4
SOURCE house mouse strain=129SVJ.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciuromorpha; Muridae; Murinae; Mus.
AUTHORS 1 (bases 1 to 710) Harding,P.A., Brigstock,D.R., Shen,L., Crissman-Combs,M.A. and Besner,G.E.
TITLE Characterization of the gene encoding murine heparin-binding epidermal growth factor-like growth factor
JOURNAL Gene 169 (2), 291-292 (1996)
MEDLINE REFERENCE 90194822
AUTHORS 2 (bases 1 to 710) Harding,P.A., Brigstock,D.R., Shen,L., Crissman-Combs,M.A. and Besner,G.E.
TITLE Direct Submission
JOURNAL Submitted (23-OCT-1995) Paul A. Harding, Pediatric Surgery, Childrens Hospital, 700 Childrens Drive, Columbus, OH 43205, USA
FEATURES source
/organism="Mus musculus"

CDS

Query Match 84.7%; Score 14.4; DB 54; Length 355;
Best Local Similarity 75.0%; Pred. No. 1.7e+03; Mismatches 0;
Matches 12; Conservativity 4; Indels 0; Gaps 0;

QY ||:||:||:||:||:||:
Db 301 TTGAGGAATGGTC 316

RESULT 23
CNS01GZU
LOCUS CNS01GZU 963 bp DNA
DEFINITION Anopheles gambiae STS T7 end of clone 07MT16 of NotreDame library from strain PEST of Anopheles gambiae (African malaria mosquito), sequence tagged site.
ACCESSION Ali43803
VERSION Ali43803.1
KEYWORDS STS
SOURCE African malaria mosquito.
ORGANISM Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culcoidea; Culicidae; Anopheles.
REFERENCE 1 (bases 1 to 963)
AUTHORS Direct Submission
TITLE Submitted (16-FEB-2000) Genoscope - Centre National de Sequencage : BP 191 91060 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
REFERENCE 2 (bases 1 to 963)
AUTHORS Roth,C.W., Breym,T., Ke,Z., Collins,F.H. and Weissbach,J.
TITLE Submitted (16-FEB-2000) BBMT, Institut Pasteur, 25, rue du Dr. Roux, Paris 75015, France
COMMENT This clone is from an A. gambiae BAC library provided by F.H. Collins and sequenced by Genoscope in collaboration with the Laboratory of Biochem. and Biol. Molec. of Insects, Institut

/strain="129SVJ"
/Job_xref="Taxon.10090"
/chromosome="18"
/notes="129SVJ mouse genomic library in the Lambda FIX II vector (U39189.1:163..208,U39189.1:412..585,U39190.1:68..245, U39191.1:155..310,135..207)"
/codon_start=1
/product="heparin-binding epidermal growth factor-like growth factor"
/protein_id="AAQ52617.1"
/db_xref="GI:1236400"
/translation="MKLPSWMLKELAAMSALVYGESERLRLGLAATSNDDPPT GSINOLIPLTGGGRADQEVQDLEFGTDNLFKAFSSKRPGQATPSPERNGKKKKKGKG KRRDPCLRKYKDQYCHGECKYLPQCRYHGHGIGLPVNPLVYDWT TYLAIVAVVLLSVCLIVLIVGILMFYHRGYDLESERVKLGWASS"
<1..134
/note="intron 4 is approximately 825 bp; heparin-binding epidermal growth factor-like growth factor"
/number=4
135..225
/number=5
/note="heparin-binding epidermal growth factor-like growth factor"
/number=5
498..>710
/number=6
/note="heparin-binding epidermal growth factor-like growth factor"
/number=6
168 c 187 g 185 t

FEATURES	Pasteur.	Location/qualifiers
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	1. . 963	/note="end : T7"
	/organism="Anopheles gambiae"	<47. .>988 similar to <i>Saccharomyces cerevisiae</i> ORF YHR005c [
	/strain="PST"	/db_xref="taxon:7165"
	/db_xref="taxon:7165"	/clone_1ib="Notredame1"
	/note="end : T7"	/evidence="not experimental pathway]"
BASE COUNT	273 a 182 c	192 g 313 t 3 others
ORIGIN		
RESULT	24	
CNS07CNO/c		
LOCUS	CNS07CNO	997 bp DNA STS
DEFINITION	T7 end of clone BD0AA04D05 of library BD0AA	from strain CBS 94 of
CANDIDA	Candida tropicalis, sequence tagged site.	
ACCESSION	AL42404	
VERSION	AL42404.1	GI:1222817
KEYWORDS	STS.	
ORGANISM	<i>Candida tropicalis</i> .	
	Eukaryote; Fungi; Ascomycota; <i>Saccharomycotina</i> ; <i>Saccharomycetes</i> ; <i>Saccharomyceales</i> ; <i>Candida</i> .	
REFERENCE	1. (bases 1 to 997)	
AUTHORS	Blandin,G., Ozier-Kalogeropoulos,O., Wincker,P., Artigueneave,F. and Dujon,B.	
TITLE	Genomic Exploration of the Hemiascomycetous Yeasts: 15. <i>Candida</i> tropicalis	
JOURNAL	FEBS Lett.	487 (1), 91-94 (2000)
PUBLMED	11152891	
REFERENCE	2. (bases 1 to 997)	
AUTHORS	Souciet,J.L., Aigle,M., Artigueneave,F., Blandin,G., Brottier,P., Casaregola,S., Boulard-Fukuhara,M., Bon,E., Brottier,P., Lepingle,A., Llorente,B., Malpertuy,A., Nevegilise,C., Ozier-Kalogeropoulos,O., Potier,S., de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B., Saurin,W., Tekka,F., Toffano-Nicieza,C., Wesolowski-Louvel,M., Wincker,P. and Weissbach,J.	
TITLE	Genomic Exploration of the Hemiascomycetous Yeasts: 1. A set of yeast species for molecular evolution studies(1)	
JOURNAL	FEBS Lett.	487 (1), 3-12 (2000)
PUBLMED	11152876	
REFERENCE	3. (bases 1 to 997)	
AUTHORS	Genoscope.	
TITLE	Direct Submission	
JOURNAL	Submitted (08-SEP-2000) Genoscope - Centre National de Sequencrage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail : secreregenoscope.cns.fr - Web : www.genoscope.cns.fr)	
COMMENT	This STS is part of a random genomic sequencing program of thirteen yeast species: <i>Saccharomyces bayanus</i> var. <i>uvarum</i> , <i>Saccharomyces exiguus</i> , <i>Saccharomyces servazzii</i> , <i>Zygosaccharomyces rouxii</i> , <i>Saccharomyces kluveri</i> , <i>Kluyveromyces thermotolerans</i> , <i>Kluyveromyces lactis</i> var. <i>lactis</i> , <i>Kluyveromyces marriani</i> var. <i>marriani</i> , <i>Pichia</i> , <i>angusta</i> , <i>Debaromyces hansenii</i> var. <i>hansenii</i> , <i>Pichia sorbitophila</i> , <i>Candida tropicalis</i> and <i>Yarrowia lipolytica</i> . Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.	
FEATURES		
source	1. .997	/organism="Candida tropicalis"
	/strain="CBS 94"	/db_xref="taxon:5482"
	/clone="AZ0AA012B01"	
FEATURES		
source		/clone="BD0AA04D05"
	/note="end : T7"	/clone_1ib="BD0AA"
		/note="similar to <i>Saccharomyces cerevisiae</i> ORF YHR005c [
		/db_xref="taxon:7165"
		/clone_1ib="Notredame1"
		/note="end : T7"
BASE COUNT	377 a	107 c 170 g 326 t 17 others
ORIGIN		
RESULT	25	
CNS07CNG/c		
LOCUS	CNS07CNG	1084 bp DNA STS
DEFINITION	T7 end of clone AZ0AA012B01 of library AZ0AA	from strain CBS 712 of
CANDIDA	<i>Kluyveromyces marxianus</i> , sequence tagged site.	
ACCESSION	AL424051	
VERSION	AL424051.1	GI:12207245
KEYWORDS	STS.	
ORGANISM	<i>Kluyveromyces marxianus</i> .	
	Eukaryote; Fungi; Ascomycota; <i>Saccharomycotina</i> ; <i>Saccharomycetes</i> ; <i>Saccharomyceales</i> ; <i>Saccharomyces</i> ; <i>Kluyveromyces</i> .	
REFERENCE	1. (bases 1 to 1084)	
AUTHORS	Llorente,B., Malpertuy,A., Blandin,G., Artigueneave,F., Wincker,P. and Dujon,B.	
TITLE	Genomic Exploration of the Hemiascomycetous Yeasts: 12. <i>Kluyveromyces marxianus</i> var. <i>marxianus</i> .	
JOURNAL	FEBS Lett.	487 (1), 71-75 (2000)
PUBLMED	11152887	
REFERENCE	2. (bases 1 to 1084)	
AUTHORS	Souciet,J.L., Aigle,M., Artigueneave,F., Blandin,G., Brottier,P., Casaregola,S., Boulard-Fukuhara,M., Bon,E., Brottier,P., Lepingle,A., Llorente,B., Malpertuy,A., Nevegilise,C., Ozier-Kalogeropoulos,O., Potier,S., de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B., Saurin,W., Tekka,F., Toffano-Nicieza,C., Wesolowski-Louvel,M., Wincker,P. and Weissbach,J.	
TITLE	Genomic Exploration of the Hemiascomycetous Yeasts: 1. A set of yeast species for molecular evolution studies(1)	
JOURNAL	FEBS Lett.	487 (1), 3-12 (2000)
PUBLMED	11152876	
REFERENCE	3. (bases 1 to 1084)	
AUTHORS	Genoscope.	
TITLE	Direct Submission	
JOURNAL	Submitted (08-SEP-2000) Genoscope - Centre National de Sequencrage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail : secreregenoscope.cns.fr - Web : www.genoscope.cns.fr)	
COMMENT	This STS is part of a random genomic sequencing program of thirteen yeast species: <i>Saccharomyces bayanus</i> var. <i>uvarum</i> , <i>Saccharomyces exiguus</i> , <i>Saccharomyces servazzii</i> , <i>Zygosaccharomyces rouxii</i> , <i>Saccharomyces kluveri</i> , <i>Kluyveromyces thermotolerans</i> , <i>Kluyveromyces lactis</i> var. <i>lactis</i> , <i>Kluyveromyces marriani</i> var. <i>marriani</i> , <i>Pichia</i> , <i>angusta</i> , <i>Debaromyces hansenii</i> var. <i>hansenii</i> , <i>Pichia sorbitophila</i> , <i>Candida tropicalis</i> and <i>Yarrowia lipolytica</i> . Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.	
FEATURES		
source	1. .1084	/organism="Kluyveromyces marxianus"
	/strain="CBS 712"	/db_xref="taxon:491"
	/clone="AZ0AA012B01"	

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BASE COUNT	/clone_11b="AZ0RA"	262 a	245 c	196 g	380 t	1 others
ORIGIN						

Query Match
Best Local Similarity 84.7%; Score 14.4; DB 53; Length 1084;
Matches 12; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TTYGARGARGARGAYC 16
|:||||:||||:||:
Db 426 TTGAGAAGATGATC 411

Search completed: May 15, 2001, 11:13:37
Job time: 3608 sec